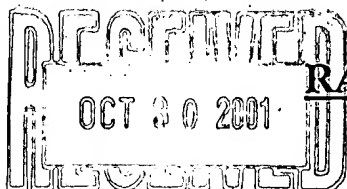


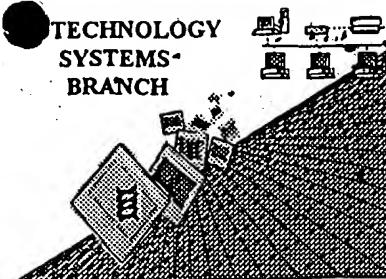
US 920  
0815



## RAW SEQUENCE LISTING ERROR REPORT

Docket System ☒  
Status Report ☒  
Docket Book ☒

TECHNOLOGY  
SYSTEMS-  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US/09/918186  
Source: OIPE  
Date Processed by STIC: 08/13/01

*Notice to Comply*  
10-23-01  
12-23-01  
MAX 4-23-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OICE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/918,186

DATE: 08/13/2001

TIME: 11:38:07

Input Set : A:\isph585seq.txt

Output Set: N:\CRF3\08132001\I918186.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: C. Frank Bennett  
 4 Elizabeth J. Ackermann  
 5 Eric E. Swayze  
 6 Lex M. Cowser  
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
 10 <130> FILE REFERENCE: ISPH-0585  
 12 <140> CURRENT APPLICATION NUMBER: US/09/918,186  
 12 <141> CURRENT FILING DATE: 2001-07-30  
 12 <150> PRIOR APPLICATION NUMBER: 92000-02-02  
 W--> 13 <151> PRIOR FILING DATE: 09/496,694  
 15 <150> PRIOR APPLICATION NUMBER: 1999-04-05  
 W--> 16 <151> PRIOR FILING DATE: 09/286,407  
 18 <150> PRIOR APPLICATION NUMBER: 1998-09-29  
 W--> 19 <151> PRIOR FILING DATE: 09/163,162  
 21 <160> NUMBER OF SEQ ID NOS: 250

Does Not Comply  
Corrected Diskette Needed

Errored: See Page 1 and 2.

1507 and 1517 responses  
are reversed; please  
edit

## ERRORED SEQUENCES

1796 <210> SEQ ID NO: 97  
 1797 <211> LENGTH: 1620  
 1798 <212> TYPE: DNA  
 1799 <213> ORGANISM: Homo sapiens  
 1802 <400> SEQUENCE: 97

E--> 1803 ccgccagatt tgaatcgcgg gaccgcttgg cagaggtggc ggccggcgga tgggtgcccc  
 E--> 1805 gacgttgccc cctgcctggc agccctttct caaggaccac cgcattctcta cattcaagaa 121  
 E--> 1807 ctggcccttc ttggagggct gcgcctgcac cccggagcgg atggccgagg ctggcttcat 181  
 E--> 1809 ccaactgcccc actgagaacg agccagactt ggcccagtgt ttcttctgct tcaaggagct 241  
 E--> 1811 ggaaggctgg gagccagatg acgaccccat agaggaaacat aaaaagcatt cgtccggttg 301  
 E--> 1813 cgttttcett tctgtcaaga agcagtttga agaattaacc cttggtgaat ttttgaaact 361  
 E--> 1815 ggacagagaa agagccaaga acaaaattgc aaaggaaacc aacaataaga agaaagaatt 421  
 E--> 1817 tgaggaaact gcgaagaaag tgcgccgtgc catcgagcag ctggctgcca tggattgagg 481  
 E--> 1819 cctctggccg gagctgcctg gtcccagagt ggctgcacca cttccagggt ttattccctg 541  
 E--> 1822 gtgccaccag ccttcctgtg ggccccttag caatgtctta ggaaaggaga tcaacatttt 601  
 E--> 1824 caaattagat gtttcaactg tgctcctgtt ttgtcttgaa agtggcacca gaggtgcttc 661  
 E--> 1826 tgccctgtgca gcgggtgctg ctggtaacag tggctgcttc tctctctctc tctctttttt 721  
 E--> 1828 gggggctcat ttttgcgtgt ttgattcccg ggcttaccag gtgagaagtg agggaggaag 781  
 E--> 1830 aaggcagtgt cccttttgcct agagctgaca gctttgttcg cgtgggcaga gccttcacaa 841  
 E--> 1832 gtgaatgtgt ctggacctca tgttgttgag gctgtcacag tcttgagtgt ggacttgga 901  
 E--> 1834 ggtgcctgtt gaacttgagc tgcaggttcc ttatctgtca cactgtgcc tctcagagg 961  
 E--> 1836 acagtttttt tgttgttggt tttttttgtt tttttttttt ggtagatgca tgacttgtgt 1021  
 E--> 1838 gtgatgagag aatggagaca gagtccctgg ctccctctact gtttaacaac atggctttct 1081  
 E--> 1840 tattttgttt gaattgttaa ttcacagaat agcacaact acaattaaaa ctaagcacia 1141  
 E--> 1842 agccattcta agtcattggg gaaacggggt gaacttcagg tggatgagga gacagaatag 1201  
 E--> 1844 agtgatagga agcgtctggc agatactcct tttgccactg ctgtgtgatt agacaggccc 1261  
 E--> 1846 agtgagccgc ggggcacatg ctggccgctc ctccctcaga aaaaggcagt ggcctaaatc 1321  
 E--> 1848 ctttttaaat gacttggctc gatgctgtgg gggactggct gggctgctgc aggccgtgtg 1381

Format Errors

Inputs are incorrect

Errored

61 60

numbering  
off

## RAW SEQUENCE LISTING

DATE: 08/13/2001

PATENT APPLICATION: US/09/918,186

TIME: 11:38:08

Input Set : A:\isph585seq.txt

Output Set: N:\CRF3\08132001\I918186.raw

E--> 1850 tctgtcagcc caaccttcac atctgtcacg ttctccacac gggggagaga cgcagtcgcg 1441  
 E--> 1852 ccaggteccc gctttctttg gaggcagcag ctcccgcagg gctgaagtct ggcgtaagat 1501  
 E--> 1854 gatggatttg attcgccctc ctccctgtca tagagctgca ggggtgattg ttacagcttc 1561  
 E--> 1856 gctggaaacc tctggaggtc atctcggctg ttctgagaa ataaaaagcc tgtcatttc 1620  
 3739 <210> SEQ ID NO: 250  
 3740 <211> LENGTH: 18  
 3741 <212> TYPE: DNA  
 3742 <213> ORGANISM: Artificial Sequence  
 3744 <220> FEATURE:  
 3745 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 3747 <400> SEQUENCE: 250  
 3748 tctgctattc tgtgaatt

18

E--&gt; 3752 59

Delete Non ASCII text

reads numeric indicator as end of ~~string~~ counter

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

09/9/8, 186

5

<210> 91

<211> 18

<212> DNA

<213> Artificial Sequence

<220> *← insert this mandatory numeric identifier wherever* <221>, <222>

<223> Antisense Oligonucleotide

*or <223> is present*

<400> 91

gaggagcggc cagcatgt

18



The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/918,186

DATE: 08/13/2001

TIME: 11:38:09

Input Set : A:\isph585seq.txt

Output Set: N:\CRF3\08132001\I918186.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD -  
 L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD -  
 L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD -  
 L:645 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:967 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1353 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1730 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:1740 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1803 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:60 SEQ:97  
 M:254 Repeated in SeqNo=97 -  
 L:1856 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1620 Found:1619 SEQ:97 ✓  
 L:2011 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2022 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2033 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2044 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2104 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2115 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:2770 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:3414 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:3499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:231  
 L:3737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249  
 L:3752 M:254 E: No. of Bases conflict, LENGTH:Input:59 Counted:18 SEQ:250